



1/7

SEQUENCE LISTING

<110> Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN

<120> Chlamydia antigens and corresponding DNA fragments and uses thereof

10 <130> 77813-49

<140> to be assigned

<141>

<150> US 60/194,464

<151> 2000-04-04

<160> 7

20 <170> PatentIn Ver. 2.0

<210> 1

<211> 1799

<212> DNA

<213> Chlamydia pneumoniae

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<221> CDS

30 <222> (101)..(1696)

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Met Arg Lys Ile Ser
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40 gtg gga atc tgt atc acc att ctc ctt agc ctc tcc gta gtc ctc caa 163
Val Gly Ile Cys Ile Thr Ile Leu Leu Ser Leu Ser Val Val Leu Gln
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ggc tgc aag gag tcc agt cac tcc tct aca tct cgg gga gaa ctc gct 211
Gly Cys Lys Glu Ser Ser His Ser Ser Thr Ser Arg Gly Glu Leu Ala
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att aat ata aga gat gaa ccc cgt tct tta gat cca aga caa gtg cga 259
Ile Asn Ile Arg Asp Glu Pro Arg Ser Leu Asp Pro Arg Gln Val Arg
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50 ctt ctt tca gaa atc agc ctt gtc aaa cat atc tat gag gga tta gtt 307
Leu Leu Ser Glu Ile Ser Leu Val Lys His Ile Tyr Glu Gly Leu Val
55 60 65

caa gaa aat aat ctt tca gga aat ata gag cct gct ctt gca gaa gac 355
Gln Glu Asn Asn Leu Ser Gly Asn Ile Glu Pro Ala Leu Ala Glu Asp
70 75 80 85

60 tac tct ctt tcc tcg gac gga ctc act tat act ttt aaa ctg aaa tca 403
Tyr Ser Leu Ser Ser Asp Gly Leu Thr Tyr Thr Phe Lys Leu Lys Ser
90 95 100

2/7

	gct ttt tgg agt aat ggc gac ccc tta aca gct gaa gac ttt ata gaa	451
	Ala Phe Trp Ser Asn Gly Asp Pro Leu Thr Ala Glu Asp Phe Ile Glu	
	105 110 115	
	tct tgg aaa caa gta gct act caa gaa gtc tca gga atc tat gct ttt	499
	Ser Trp Lys Gln Val Ala Thr Gln Glu Val Ser Gly Ile Tyr Ala Phe	
	120 125 130	
10	gcc ttg aat cca att aaa aat gta cga aag atc caa gag gga cac ctc	547
	Ala Leu Asn Pro Ile Lys Asn Val Arg Lys Ile Gln Glu Gly His Leu	
	135 140 145	
	tcc ata gac cat ttt gga gtg cac tct cct aat gaa tct aca ctt gtt	595
	Ser Ile Asp His Phe Gly Val His Ser Pro Asn Glu Ser Thr Leu Val	
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20	gtt acc ctg gaa tcc cca acc tcg cat ttc tta aaa ctt tta gct ctt	643
	Val Thr Leu Glu Ser Pro Thr Ser His Phe Leu Lys Leu Leu Ala Leu	
	170 175 180	
	cca gtc ttt ttc ccc gtt cat aaa tct caa aga acc ctg caa tcc aaa	691
	Pro Val Phe Phe Pro Val His Lys Ser Gln Arg Thr Leu Gln Ser Lys	
	185 190 195	
	tct cta cct ata gca agc gga gct ttc tat cct aaa aat atc aaa caa	739
	Ser Leu Pro Ile Ala Ser Gly Ala Phe Tyr Pro Lys Asn Ile Lys Gln	
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30	aaa caa tgg ata aaa ctc tca aaa aac cct cac tac tat aat caa agt	787
	Lys Gln Trp Ile Lys Leu Ser Lys Asn Pro His Tyr Tyr Asn Gln Ser	
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	cag gtg gaa act aaa acg att acg att cac ttc att ccc gat gca aac	835
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	230 235 240 245	
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	Thr Ala Ala Lys Leu Phe Asn Gln Gly Lys Leu Asn Trp Gln Gly Pro	
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	cct tgg gga gaa cgc att cct caa gaa acc cta tcc aat tta cag tct	931
	Pro Trp Gly Glu Arg Ile Pro Gln Glu Thr Leu Ser Asn Leu Gln Ser	
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	aag ggg cac tta cac tct ttt gat gtc gca gga acc tca tgg ctc acc	979
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	Phe Asn Ile Asn Lys Phe Pro Leu Asn Asn Met Lys Leu Arg Glu Ala	
	295 300 305	
	tta gca tca gcc tta gat aag gaa gct ctt gtc tca act ata ttc tta	1075
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60	ggc cgt gca aaa act gcc gat cat ctc cta cct aca aat att cat agc	1123
	Gly Arg Ala Lys Thr Ala Asp His Leu Leu Pro Thr Asn Ile His Ser	
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3/7

	tat ccc gaa cat caa aaa caa gag atg gca caa cgc caa gct tac gct	1171
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	aaa aaa ctc ttt aaa gaa gct tta gaa gaa ctc caa atc act gct aaa	1219
	Lys Lys Leu Phe Lys Glu Ala Leu Glu Glu Leu Gln Ile Thr Ala Lys	
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	tct tta cta gtc caa ctt ata cga gaa cag tgg aaa gaa agt tta ggg	1315
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	Leu Ser Ser Gly Asn Phe Ser Leu Ala Thr Gly Gly Trp Phe Ala Asp	
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	Phe Ala Asp Pro Met Ala Phe Leu Thr Ile Phe Ala Tyr Pro Ser Gly	
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30	gtt cct cct tat gca atc aac cat aag gac ttc cta gaa att cta caa	1507
	Val Pro Pro Tyr Ala Ile Asn His Lys Asp Phe Leu Glu Ile Leu Gln	
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	aac ata gaa caa gag caa gat cac caa aaa cgc tcg gaa tta gtg tcg	1555
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40	caa gct tct ctt tac cta gag acc ttt cat att att gag ccg atc tac	1603
	Gln Ala Ser Leu Tyr Leu Glu Thr Phe His Ile Ile Glu Pro Ile Tyr	
	490 495 500	
	cac gac gca ttt caa ttt gct atg aat aaa aaa ctt tct aat cta gga	1651
	His Asp Ala Phe Gln Phe Ala Met Asn Lys Lys Leu Ser Asn Leu Gly	
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	Val Ser Pro Thr Gly Val Val Asp Phe Arg Tyr Ala Lys Glu Asn	
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<222> (53)...(61)
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35 40 45

Pro Arg Gln Val Arg Leu Leu Ser Glu Ile Ser Leu Val Lys His Ile
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30 Tyr Glu Gly Leu Val Gln Glu Asn Asn Leu Ser Gly Asn Ile Glu Pro
65 70 75 80

Ala Leu Ala Glu Asp Tyr Ser Leu Ser Ser Asp Gly Leu Thr Tyr Thr
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Phe Lys Leu Lys Ser Ala Phe Trp Ser Asn Gly Asp Pro Leu Thr Ala
100 105 110

Glu Asp Phe Ile Glu Ser Trp Lys Gln Val Ala Thr Gln Glu Val Ser
115 120 125

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Gly Ile Tyr Ala Phe Ala Leu Asn Pro Ile Lys Asn Val Arg Lys Ile
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Gln Glu Gly His Leu Ser Ile Asp His Phe Gly Val His Ser Pro Asn
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Glu Ser Thr Leu Val Val Thr Leu Glu Ser Pro Thr Ser His Phe Leu
165 170 175

50 Lys Leu Leu Ala Leu Pro Val Phe Phe Pro Val His Lys Ser Gln Arg
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Thr Leu Gln Ser Lys Ser Leu Pro Ile Ala Ser Gly Ala Phe Tyr Pro
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Lys Asn Ile Lys Gln Lys Gln Trp Ile Lys Leu Ser Lys Asn Pro His
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60 Tyr Tyr Asn Gln Ser Gln Val Glu Thr Lys Thr Ile Thr Ile His Phe
225 230 235 240

Ile Pro Asp Ala Asn Thr Ala Ala Lys Leu Phe Asn Gln Gly Lys Leu
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Asn Trp Gln Gly Pro Pro Trp Gly Glu Arg Ile Pro Gln Glu Thr Leu
260 265 270

10 Ser Asn Leu Gln Ser Lys Gly His Leu His Ser Phe Asp Val Ala Gly
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Thr Ser Trp Leu Thr Phe Asn Ile Asn Lys Phe Pro Leu Asn Asn Met
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Lys Leu Arg Glu Ala Leu Ala Ser Ala Leu Asp Lys Glu Ala Leu Val
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20 Ser Thr Ile Phe Leu Gly Arg Ala Lys Thr Ala Asp His Leu Leu Pro
325 330 335

Thr Asn Ile His Ser Tyr Pro Glu His Gln Lys Gln Glu Met Ala Gln
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Arg Gln Ala Tyr Ala Lys Lys Leu Phe Lys Glu Ala Leu Glu Glu Leu
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Gln Ile Thr Ala Lys Asp Leu Glu His Leu Asn Leu Ile Phe Pro Val
370 375 380

30 Ser Ser Ser Ala Ser Ser Leu Leu Val Gln Leu Ile Arg Glu Gln Trp
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40 Gly Trp Phe Ala Asp Phe Ala Asp Pro Met Ala Phe Leu Thr Ile Phe
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Ala Tyr Pro Ser Gly Val Pro Pro Tyr Ala Ile Asn His Lys Asp Phe
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Ile Glu Pro Ile Tyr His Asp Ala Phe Gln Phe Ala Met Asn Lys Lys
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Ala Lys Glu Asn
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7/7

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Arg Leu Leu Ser Glu Ile Ser Leu Val

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